Pcf/10

CRF Errors Edited by the STIC Systems Branch

Serial	Number: <u>/0/506,406</u>	CRF Edit Date:Edited by:	9/13/04
1300 200	Realigned multiple remaining add numbers/text text "wrapped to the next ine Corrected the SEQ ID NO. Sequence numbers of	in cases where the	sequence
no rec	Inserted or corrected a nucleic number at the en NO's edited:	d of a nucleic line.	SEQ ID
	Deleted: invalid beginning/end-of-file text;	page numbers	
	Inserted mandatory headings/numeric identifier Moved responses to same line as heading/numer		ically:
	Other: replaced "Home sapiens" with "Ho	omo Sapiens' (ga	lobally)



PCT

RAW SEQUENCE LISTING DATE: 09/13/2004
PATENT APPLICATION: US/10/506,406 TIME: 16:34:52

Input Set : N:\AMC\506406.txt

```
4 <110> APPLICANT: Swiercz, Rafal
             Selman, Steven
      5
              Jankun, Jerzy
     6
     7
              Chorostowska-Wynimko, Joanna
              Skrzypczak-Jankun, Ewa
     10 <120> TITLE OF INVENTION: MODIFIED PLASMINOGEN ACTIVATOR INHIBITOR
    11
              TYPE-1 AND METHODS BASED THEREON
     14 <130> FILE REFERENCE: 9471-011-999
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/506,406
C--> 17 <141> CURRENT FILING DATE: 2004-09-01
    19 <150> PRIOR APPLICATION NUMBER: PCT/US03/06679
    20 <151> PRIOR FILING DATE: 2003-03-04
    22 <150> PRIOR APPLICATION NUMBER: 60/361,670
    23 <151> PRIOR FILING DATE: 2002-03-04
    25 <160> NUMBER OF SEQ ID NOS: 3
    27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    29 <210> SEQ ID NO: 1
    30 <211> LENGTH: 2876
    31 <212> TYPE: DNA
    32 <213> ORGANISM: Homo sapiens
    34 <220> FEATURE:
    35 <221> NAME/KEY: CDS
    36 <222> LOCATION: (76)...(1281)
    37 <223> OTHER INFORMATION: human PAI-1 plus 5' and 3' sequence
    39 <400> SEQUENCE: 1
     40 gaatteetge ageteageag cegeegeeag ageaggaega acegeeaate geaaggeace 60
    41 totgagaact toagg atg cag atg tot coa goo oto acc tgo ota gto otg
    42
                         Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu
    43
    45 ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca
    46 Gly Leu Ala Leu Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro
     49 too tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag
    50 Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln
    53 cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat
    54 Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr
                             50
                                                 55
                                                                      60
    57 ggg gtg gcc tcg gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa
                                                                           303
    58 Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu
                         65
    61 acc cag cag att caa gca gct atg gga ttc aag att gat gac aag
    62 Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys
```

Input Set : N:\AMC\506406.txt

63				80					85					90			
63	aaa	ata	acc		acc	ctc	caa	cat	ctg	tac	aad	gag	ctc		aaa	cca	399
									Leu								373
67	Gry	Mec	95	110	ALU	пси	nr 9	100	Lcu	- 7 -	шуо	Olu	105		0 - <i>y</i>	110	
	taa	aac		gat	aaa	atc	agc		aca	gac	aca	atc		atc	cag	caa	447
									Thr								
71	115	110	7,5	nop	014	110	115			1100	1114	120				3	
_	gat		aag	cta	atc	сап		ttc	atg	כככ	cac		tta	agg	cta	ttc	495
									Met								
	125	пси	L , 5	шси	• • • • • • • • • • • • • • • • • • • •	130	0-1				135			3		140	
_		agc	acq	atc	aad		ata	gac	ttt	tica		at.a	gag	aga	acc		543
									Phe								
79	**** 9	DCI	1111	· · · ·	145	0111	•	1.05		150	414		020,	9	155	9	
-	ttc	atc	atc	aat		taa	ata	aaq	aca		aca	aaa	aat.	ata		agc	591
									Thr								
83	1110			160					165			-1-	J-1	170			
	aac	t.t.a	ctt		aaa	gga	acc	ata	gac	caq	cta	aca	caa		ata	cta	639
									Asp								
87			175	1	-1-	2		180		-			185				
	ata	aat		ctc	tac	ttc	aac		cag	taa	aaq	act		ttc	ccc	qac	687
			_						Gln								
91		190			- 2 -		195	-		-	-	200				-	
	tcc		acc	cac	cqc	các	ctc	ttc	cac	aaa	tca	qac	qqc	agc	act	gtc	735
									His								
	205					210				•	215	-	-			220	
97	tct	qtq	ccc	atq	atq	qct	caq	acc	aac	aaq	ttc	aac	tat	act	gag	ttc	783
									Asn								
99					225					230			-		235		
10	1 acc	acg	g ccc	gat	ggd	cat	tac	: ta	gac	ato	cto	g gaa	a cto	g cc	c ta	c cac	831
10	2 Thi	r Thi	r Pro	Asp	Gly	His	ту1	Ty:	r Asp	Ile	e Lei	ı Glı	ı Leı	ı Pro	Ty:	r His	
10	3			240)				245	5				250)		
10	5 ggg	g gad	c acc	cto	ago	ato	, ttc	att	t gct	gc	c cct	tat	gaa	a aaa	a ga	g gtg	879
10	6 Gly	/ Asp	o Thi	r Lei	ı Ser	Met	Phe	e Ile	e Ala	a Ala	a Pro	o Ty	r Glı	ı Lys	s Glı	u Val	
10	7		255	5				26	0				265	5			
																c cac	927
11	0 Pro) Let	ı Sei	r Ala	ı Leı	Thr	Asr	ılle	e Lev	ı Sei	: Ala	a Gli	ı Lei	ı Ile	e Se:	r His	
11		270					275					280					
																c aag	975
11	4 Trp	, Lys	s Gly	y Asr	ı Met	Thr	Arc	j Lei	ı Pro	Arg	J Leι	ม Leเ	ı Val	. Le	ı Pro	o Lys	
	5 285					290					295					300	
																cctg	1023
11	B Phe	e Sei	r Lei	ı Glu	ı Thr	Glu	ı Val	. Asj	o Lev			s Pro	o Lei	ı Glı		n Leu	
11			,		305					310					31		
																t ctt	1071
12	2 Gly	/ Met	Thi	Asp	Met	Phe	e Arc	g Gli	n Phe	e Glr	ı Ala	a Asp	Phe	Thi	s Se	r Leu	
12				320					325					330			
																g aag	1119
12	Sei	: Asp	Glr	ı Glu	ı Pro	Leu	ı His			Glr	ı Ala	a Lei			s Vai	l Lys	
12	7		335	5				340)				345	5			

Input Set : N:\AMC\506406.txt

```
1167
129 atc gag gtg aac gag agt ggc acg gtg gcc tcc tca tcc aca gct gtc
130 Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val
                          355
133 ata gtc tca gcc.cgc atg gcc ccc gag gag atc atc atg gac aga ccc
                                                                   1215
134 Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro
                                                           . 380
135 365
                       370
                                          375
137 ttc ctc ttt gtg gtc cgg cac aac ccc aca gga aca gtc ctt ttc atg
                                                                   1263
138 Phe Leu Phe Val Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met
                   385
                                      390
                                                                   1311
141 ggc caa gtg atg gaa ccc tgaccctggg gaaagacgcc ttcatctggg
142 Gly Gln Val Met Glu Pro
145 acaaaactgg agatgcatcg ggaaagaaga aactccgaag aaaagaattt tagtgttaat 1371
146 gactetttet gaaggaagag aagacatttg cettttgtta aaagatggta aaccagatet 1431
147 gtctccaaga ccttggcctc tccttggagg acctttaggt caaactccct agtctccacc 1491
148 tgagaccetg ggagagaagt ttgaagcaca acteeettaa ggteteeaaa ceagaeggtg 1551
149 acgcctgcgg gaccatctgg ggcacctgct tccacccgtc tctctgccca ctcgggtctg 1611
150 caqacctggt tcccactgag gccctttgca ggatggaact acggggctta caggagcttt 1671
151 tgtgtgcctg gtagaaacta tttctgttcc agtcacattg ccatcactct tgtactgcct 1731
152 gccaccgcgg aggaggctgg tgacaggcca aaggccagtg gaagaaacac cctttcatct 1791
153 cagagtecae tgtggcaetg gecaeceete eccagtaeag gggtgetgea ggtggeagag 1851
155 agtgtgcatg ggttattttg gagtgtaggt gacttgttta ctcattgaag cagatttctg 1971
156 cttcctttta tttttatagg aatagaggaa gaaatgtcag atgcgtgccc agctcttcac 2031
157 cccccaatct cttggtgggg aggggtgtac ctaaatattt atcatatcct tgcccttgag 2091
158 tgcttgttag agagaaagag aactactaag gaaaataata ttatttaaac tcgctcctag 2151
159 tgtttctttg tggtctgtgt caccgtatct caggaagtcc agccacttga ctggcacaca 2211
160 cccctccgga catccagcgt gacggagccc acactgccac cttgtggccg cctgagaccc 2271
161 tegegeeece egegeeece gegeeeetet titteeeett gatggaaatt gaeeatacaa 2331
162 tttcatcctc cttcagggga tcaaaaggac ggagtggggg gacagagact cagatgagga 2391
163 cagagtggtt tccaatgtgt tcaatagatt taggagcaga aatgcaaggg gctgcatgac 2451
164 ctaccaggac agaactttcc ccaattacag ggtgactcac agccgcattg gtgactcact 2511
165 tcaatgtgtc atttccggct gctgtgtgtg agcagtggac acgtgagggg ggggtgggtg 2571
166 agagagacag gcagctcgga ttcaactacc ttagataata tttctgaaaa cctaccagcc 2631
167 agagggtagg gcacaaagat ggatgtaatg cactttggga ggccaaggcg ggaggattgc 2691
168 ttgagcccag gagttcaaga ccagcctggg caacatacca agacccccgt ctctttaaaa 2751
170 attttaaaga ccaatttatg ggagaattgc acacagatgt gaaatgaatg taatctaata 2871
                                                                   2876
171 gaagc
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 402
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <220> FEATURE:
179 <223> OTHER INFORMATION: human PAI-1 amino acid sequence, including signal peptide
181 <400> SEQUENCE: 2
182 Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu
184 Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala
```

Input Set : N:\AMC\506406.txt

									0.5					2.0		
185		_		20	_	-1	~7		25	** . 7	51.	~ 1.	~ 1	30		~ 1
	HIS	Leu		ser	Asp	Pne	GIY	Val	Arg	vaı	Pne	Gin		vaı	Ата	GIn
187		_	35		_	_	-	40		_	_	_	45			_
	Ala		Lys	Asp	Arg	Asn		Val	Phe	Ser	Pro		Gly	Val	Ala	Ser
189		50				_	55	_	_	_	•_	60				
		Leu	Ala	Met	Leu		Leu.	Thr	Thr	Gly	_	Glu	Thr	Gln	Gln	Gln
191						70					75					80
192	Ile	Gln	Ala	Ala	Met	Gly	Phe	Lys	Ile	Asp	Asp	Lys	Gly	Met	Ala	Pro
193					85					90					95	
194	Ala	Leu	Arg	His	Leu	Tyr	Lys	Glu	Leu	Met	Gly	Pro	Trp	Asn	Lys	Asp
195			,	100					105					110		
196	Glu	Ile	Ser	Thr	Thr	Asp	Ala	Ile	Phe	Val	Gln	Arg	Asp	Leu	Lys	Leu
197			115					120					125			
198	Val	Gln	Gly	Phe	Met	Pro	His	Phe	Phe	Arg	Leu	Phe	Arg	Ser	Thr	Val
199		130					135					140				
200	Lys	Gln	Val	Asp	Phe	Ser	Glu	.Val	Glu	Arg	Ala	Arg	Phe	Ile	Ile	Asn
201	145					150					155					160
202	Asp	Trp	Val	Lys	Thr	His	Thr	Lys	Gly	Met	Ile	Ser	Asn	Leu	Leu	Gly
203					165					170					175	
204	Lys	Gly	Ala	Val	Asp	Gln	Leu	Thr	Arg	Leu	Val	Leu	Val	Asn	Ala	Leu
205				180					185					190		
206	Tyr	Phe	Asn	Gly	Gln	Trp	Lys	Thr	Pro	Phe	Pro	Asp	Ser	Ser	Thr	His
207	_		195	_				200					205			
208	Arg	Arg	Leu	Phe	His	Lys	Ser	Asp	Gly	Ser	Thr	Val	Ser	Val	Pro	Met
209	_	210				_	215	_	_			220				
210	Met	Ala	Gln	Thr	Asn	Lys	Phe	Asn	Tyr	Thr	Glu	Phe	Thr	Thr	Pro	Asp
	225					230			-		235					240
212	Gly	His	Tyr	Tyr	Asp	Ile	Leu	Glu	Leu	Pro	Tyr	His	Gly	Asp	Thr	Leu
213	•		•	•	245					250	-		-	-	255	
214	Ser	Met	Phe	Ile	Ala	Ala	Pro	Tyr	Glu	Lys	Glu	Val	Pro	Leu	Ser	Ala
215				260				•	265	•				270		
216	Leu	Thr	Asn	Ile	Leu	Ser	Ala	Gln	Leu	Ile	Ser	His	Trp	Lys	Gly	Asn
217			275					280					285	•	•	
	Met	Thr	Arq	Leu	Pro	Arq	Leu	Leu	Val	Leu	Pro	Lys	Phe	Ser	Leu	Glu
219		290					295					300				
	Thr	Glu	Val	Asp	Leu	Ara		Pro	Leu	Glu	Asn	Leu	Glv	Met	Thr	Asp
	305					310	-1-			,	315		2			320
		Phe	Ara	Gln	Phe		Ala	Asp	Phe	Thr		Leu	Ser	Asp	Gln	
223			3		325			1		330					335	
	Pro	Len	His	Val		Gln	Ala	Leu	Gln		Val	Lvs	Ile	Glu		Asn
225				340					345	-1-		-1		350		
	Glu	Ser	Glv		Val	Ala	Ser	Ser		Thr	Ala	Val	Tle		Ser	Ala
227		DCI	355		•	711u	501	360	001			• • • •	365		001	
		Met		Pro	Glu	Glu	Tle	Ile	Met	Asn	Ara	Pro		Len	Phe	Val
229	_	370	miu	110	Gru	υ ₁ u	375	110		p	**** 9	380		 _u	1.10	
			Hie	Aen	Dro	Thr		Thr	va 1	T.e.:	Phe		Glv	Gln	٧a٦	Met
	385	Arg	1113	VOII	.10	390	O L Y	1111	Val	u⊂u	395	1100	O L y	O 1 11	V 44.1	400
	Glu	Dro				230					دود					
	<210		יז הב	א ה	. 2											
233	<21	J > 51	יע או	טא כ	د .											

Input Set : N:\AMC\506406.txt

	36 <211> LENGTH: 379															
	<212> TYPE: PRT <213> ORGANISM: Homo sapiens															
					Homo	sap	piens	5								
	<220															
	<22					rion:	: hur	nan I	PAI-I	L mat	cure	amir	no ac	cid s	seque	ence
	<40		~						_			_				
244	Val	His	His	Pro	Pro	Ser	Tyr	Val	Ala		Leu	Ala	Ser	Asp		Gly
245				•	5					10					15	_
246	Val	Arg	Val	Phe	Gln	Gln	Val	Ala	Gln	Ala	Ser	Lys	Asp		Asn	Val
247				20					25					30	_	
248	Val	Phe	Ser	Pro	Tyr	Gly	Val	Ala	Ser	Val	Leu	Ala		Leu	Gln	Leu
249			35					40					45			
250	Thr	Thr	Gly	Gly	Glu	Thr	Gln	Gln	Gln	Ile	Gln	Ala	Ala	Met	Gly	Phe
251		50					55					60				
252	Lys	Ile	Asp	Asp	Lys	Gly	Met	Ala	Pro	Ala	Leu	Arg	His	Leu	Tyr	Lys
253						70					75					80
254	Glu	Leu	Met	Gly	Pro	\mathtt{Trp}	Asn	Lys	Asp	Glu	Ile	Ser	Thr	Thr	Asp	Ala
255				•	85					90					95	
256	Ile	Phe	Val	Gln	Arg	Asp	Leu	Lys	Leu	Val	Gln	Gly	Phe	Met	Pro	His
257				100					105					110		
258	Phe	Phe	Arg	Leu	Phe	Arg	Ser	Thr	Val	Lys	Gln	Val	Asp	Phe	Ser	Glu
259			115					120					125			
260	Val	Glu	Arg	Ala	Arg	Phe	Ile	Ile	Asn	Asp	Trp	Val	Lys	Thr	His	Thr
261		130					135					140				
262	Lys	Gly	Met	Ile	Ser	Asn	Leu	Leu	Gly	Lys	Gly	Ala	Val	Asp	Gln	Leu
263	145					150					155					160
264	Thr	Arg	Leu	Val	Leu	Val	Asn	Ala	Leu	Tyr	Phe	Asn	Gly	Gln	Trp	Lys
265					165					170					175	
266	Thr	Pro	Phe	Pro	Asp	Ser	Ser	Thr	His	Arg	Arg	Leu	Phe	His	Lys	Ser
267				180					185					190		
268	Asp	Gly	Ser	Thr	Val	Ser	Val	Pro	Met	Met	Ala	Gln	Thr	Asn	Lys	Phe
269			195					200					205			
270	Asn	Tyr	Thr	Glu	Phe	Thr	Thr	Pro	Asp	Gly	His	Tyr	Tyr	Asp	Ile	Leu
271		210					215					220				
272	Glu	Leu	Pro	Tyr	His	Gly	Asp	Thr	Leu	Ser	Met	Phe	Ile	Ala	Ala	Pro
	225					230					235					240
274	Tyr	Glu	Lys	Glu	Val	Pro	Leu	Ser	Ala	Leu	Thr	Asn	Ile	Leu	Ser	Ala
275					245					250					255	
276	Gln	Leu	Ile	Ser	His	Trp	Lys	Gly	Asn	Met	Thr	Arg	Leu	Pro	Arg	Leu
277				260					265					270		
278	Leu	Val	Leu	Pro	Lys	Phe	Ser	Leu	Glu	Thr	Glu	Val	Asp	Leu	Arg	Lys
279			275					280		1			285			
280	Pro	Leu	Glu	Asn	Leu	Gly	Met	Thr	Asp	Met	Phe	Arg	Gln	Phe	Gln	Ala
281		290					295					300				
282	Asp		Thr	Ser	Leu	Ser	Asp	Gln	Glu	Pro	Leu	His	Val	Ala	Gln	Ala
	305					310	_	•			315					320
	Leu		Lys	Val	Lys	Ile	Glu	Val	Asn	Glu	Ser	Gly	Thr	Val	Ala	Ser
285			-		325					330		-			335	
	~	Sor	Thr	Δla	Val	Tle	Val	Ser	Ala	Ara	Met	Ala	Pro	Glu	Glu	Ile

VERIFICATION SUMMARY

DATE: 09/13/2004

PATENT APPLICATION: US/10/506,406

TIME: 16:34:53

Input Set : N:\AMC\506406.txt

Output Set: N:\CRF4\09132004\J506406.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date